What is claimed is:

1. An isolated polynucleotide sequence comprising a functional vascular tissue-specific *E. grandis* cOMT promoter.

2. An isolated polynucleotide sequence comprising a sequence selected from the group consisting of:

   (a) the sequences recited in SEQ ID NO: 12 and SEQ ID NO: 113, nucleotides 1019-1643 and their complements;

   (b) reverse complements and reverse sequences of the sequences recited in (a);

   (c) sequences having at least 75% identity to a sequence recited in (a);

   (d) sequences having at least 90% identity to a sequence recited in (a);

   (e) a polynucleotide sequence that is substantially complementary to a sequence in (a) and hybridizes to said sequence under stringent conditions; and

   (f) a polynucleotide comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer, a 300-mer, 400-mer, 500-mer or 600-mer of a sequence recited in (a) or (d) above.

3. A genetic construct comprising a polynucleotide sequence selected from the group consisting of sequences recited in Claim 1 above and the sequence identified as SEQ ID NO: 60.

4. A genetic construct comprising, in the 5'-3'direction:

   (a) a promoter sequence;

   (b) a DNA sequence of interest; and

   (c) a gene termination sequence,

   wherein the promoter sequence comprises SEQ ID NO: 12 or SEQ ID NO: 113, nucleotides 1019-1643.

5. The genetic construct of claim 4, wherein the DNA sequence of interest is operably linked to the promoter in an antisense orientation.

6. The genetic construct of claim 4, wherein the DNA sequence of interest is a coding sequence operably linked to the promoter in a sense orientation.

7. The genetic construct of claim 4, wherein the DNA sequence of interest is a coding sequence present in sense and antisense orientations in the construct.

8. The genetic construct of claim 4, wherein the DNA sequence of interest comprises a non-coding sequence operably linked to the promoter in a sense orientation.

9. A genetic construct comprising in the 5'-3' direction:

(a) a promoter sequence;

(b) a polynucleotide sequence of claim 1: and

(c) a gene termination sequence,

wherein the promoter sequence in (a) comprises a xylem-specific promoter sequence that is different from the polynucleotide sequence of (b), and said polynucleotide sequence of (b) is inserted in said construct as a direct or inverted repeat.

10. A host cell comprising the genetic construct of claim 4 or claim 8.

11. The host cell of claim 9, wherein the cell is a plant cell.

12. A plant comprising a genetic construct of claim 4 or claim 8.

13. A method for producing a plant with modified gene expression, comprising:

(a) stably incorporating into the genome of the plant a genetic construct of claim 4 or claim 8.

14. A method for producing a plant having modified gene expression, comprising:

(a) transforming a plant cell with a genetic construct of claim 4, wherein the DNA sequence of interest is a coding sequence;

(b) cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth; and

(c) selecting plants that show upregulated or downregulated expression of the DNA sequence of interest as compared with a plant that has not been transgenically modified.

15. A method for identifying a gene responsible for a desired function or phenotype, comprising:

(a) transforming a plant cell with a genetic construct comprising a polynucleotide sequence of claim 2;

(b) cultivating the plant cell under conditions conducive to regeneration and mature plant growth to provide a transgenic plant; and

(c) comparing the phenotype of the transgenic plant with the phenotype of a non-transformed plant,

wherein the gene encodes a polypeptide involved in secondary cell wall formation.